

Application No.: 10/081,872

7

Docket No.: 564462006100

Amendment to the Claims:

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Please cancel claims 5, 13, 18, 81-83 and 87, without prejudice or disclaimer.

Listing of Claims:

Claim 1 (Currently amended): An isolated or recombinant nucleic acid comprising a sequence that encodes a polypeptide having alpha amylase activity, wherein said sequence is selected from the group consisting of:

- (a) a sequence having at least 85% sequence identity to a sequence as set forth in SEQ ID NO:125 over a region of at least about 100 consecutive residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and
- (b) sequences complementary to (a).

Claim 2 (Currently amended): An isolated or recombinant nucleic acid encoding a polypeptide having alpha amylase activity that hybridizes under stringent conditions to a sequence selected from the group consisting of:

- (a) a sequence encoding a polypeptide having alpha amylase activity having at least 85% sequence identity to a sequence as set forth in SEQ ID NO:125 over a region of at least about 100 residues; and,
- (b) sequences complementary to (a)

wherein the stringent conditions comprise a wash step comprising 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution at Tm-10°C, and wherein the sequence encodes a polypeptide having alpha amylase activity.

Claim 3 (Currently amended): An isolated or recombinant nucleic acid encoding a polypeptide having alpha amylase activity that hybridizes under stringent conditions to a sequence selected from the group consisting of: (a) a sequence as set forth in SEQ ID NO:125; and, (b)

sd-215892

Application No.: 10/081,872

8

Docket No.: 564462006100

sequences complementary to (a); wherein the stringent conditions comprise a wash step comprising 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution at Tm-10°C,
and wherein the sequence encodes a polypeptide having alpha amylase activity.

Claim 4 (Previously presented): The isolated or recombinant nucleic acid of claim 2 or claim 3, wherein the $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the nucleic acid.

Claim 5 (Canceled)

Claim 6 (Currently amended): The isolated or recombinant nucleic acid of claim [[5]] 1, wherein the sequence identity is determined over the entire sequence.

Claim 7 (Currently amended): The isolated or recombinant nucleic acid of claim [[5]] 2, wherein the sequence identity is determined has at least 90% sequence identity over a region of at least about 200, 300, 400 or 500 consecutive residues.

Claim 8 (Currently amended): The isolated or recombinant nucleic acid of claim [[7]] 2, wherein the sequence identity is determined has at least 95% sequence identity over a region of at least about [[400]] 75, 100, or 150 consecutive residues.

Claim 9 (Currently amended): The isolated or recombinant nucleic acid of claim [[8]] 2, wherein the sequence identity is determined has at least 97% sequence identity over a region of at least about [[500]] 50, 75, 100 or 150 consecutive residues.

Claim 10 (Currently amended): An isolated or recombinant nucleic acid comprising a sequence that encodes a polypeptide having alpha amylase activity, wherein said sequence is selected from the group consisting of: (a) a sequence having at least [[85%]] 95% sequence identity

sd-215892

Application No.: 10/081,872

9

Docket No.: 564462006100

to a sequence as set forth in SEQ ID NO:125 over a region of at least about [[35]] 75, 100, or 150 consecutive residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and (b) sequences complementary to (a).

Claim 11 (Currently amended): An isolated or recombinant nucleic acid comprising a sequence that encodes a polypeptide having alpha amylase activity, wherein the sequence is selected from the group consisting of: (a) a sequence having at least [[85%]] 97% sequence identity to a sequence as set forth in SEQ ID NO:125 over a region of at least about [[40]] 50, 75, 100 or 150 consecutive residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and (b) sequences complementary to (a).

Claim 12 (Currently amended): An isolated or recombinant nucleic acid comprising a sequence that encodes a polypeptide having alpha amylase activity, wherein the sequence is selected from the group consisting of: (a) a sequence having at least [[85%]] 90% sequence identity to a sequence as set forth in SEQ ID NO:125 over a region of at least about [[50]] 200, 300, 400 or 500 consecutive residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and (b) sequences complementary to (a).

Claim 13 (Canceled)

Claim 14 (Currently amended): The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about [[90%]] 97%.

Claim 15 (Previously presented): The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 95%.

Claim 16 (Previously presented): The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is FASTA version 3.0t78 with the default parameters.

sd-215892

Application No.: 10/081,872

10

Docket No.: 564462006100

Claim 17 (Currently amended): A ~~An isolated or recombinant nucleic acid probe comprising a nucleic acid comprising at least [[35]] 500 consecutive bases of a sequence as set forth in claim 1 or claim 2.~~

Claims 18 to 46 (Canceled)

Claim 47 (Currently amended): A method of producing a polypeptide having an amino acid sequence having at least about [[90%]] 75% sequence identity to a sequence as set forth in SEQ ID NO:126 ~~over a region of at least about 75 residues~~, as determined by analysis with a sequence comparison algorithm or by visual inspection;

~~comprising the steps of introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide, wherein the expressed polypeptide has alpha amylase activity.~~

Claim 48 (Previously presented): A method of producing a polypeptide having amylase activity, comprising the steps of: providing a nucleic acid having a sequence as set forth in claim 1, 10 or 12; introducing the nucleic acid encoding the polypeptide, operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide.

Claims 49 to 73 (Canceled)

Claim 74 (Currently amended): An assay for identifying a polypeptide having amylase activity comprising the steps of:

- (a) providing a nucleic acid as set forth in claim 1, 10 or 12
- (b) expressing the nucleic acid to provide a polypeptide;
- (c) contacting the polypeptide, with a substrate molecule under conditions which allow the polypeptide to function; and

sd-215892

Application No.: 10/081,872

11

Docket No.: 564462006100

(d) detecting either a decrease in an amount of a substrate or an increase in an amount of a reaction product which results from a reaction between said polypeptide and said substrate; wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product is indicative of existence of the functional polypeptide.

Claim 75 (Currently amended): A nucleic acid probe comprising an oligonucleotide at least about [[35]] 50 nucleotides in length and having a segment of at least [[35]] 50 contiguous nucleotides of a nucleic acid target region having sequence as set forth in claim 10; and which hybridizes under stringent conditions to the nucleic acid target region to form a detectable target:probe duplex, wherein the nucleic acid target encodes a polypeptide having alpha amylase activity and the stringent hybridization conditions comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution.

Claim 76 (Currently amended): The nucleic acid probe of claim [[74]] 75, wherein the oligonucleotide comprises DNA or RNA.

Claim 77 (Currently amended): The nucleic acid probe of claim [[74]] 75, wherein the oligonucleotide has at least [[90%]] 98% sequence identity to the nucleic acid target region.

Claim 78 (Currently amended): The nucleic acid probe of claim [[76]] 77, wherein the oligonucleotide has at least 75, 100, 150 or 200 contiguous nucleotides having at least 95% sequence identity to the nucleic acid target region.

Claim 79 (Currently amended): The nucleic acid probe of claim [[77]] 78, wherein the oligonucleotide has at least 97% sequence identity to the nucleic acid target region.

sd-215892

Application No.: 10/081,872

12

Docket No.: 564462006100

Claim 80 (Currently amended): The nucleic acid probe of claim [[78]] 75, wherein the oligonucleotide has at least [[40]] 200, 300, 400 or 500 contiguous nucleotides having at least 90% sequence identity to the nucleic acid target region.

Claims 81-83 (Canceled)

Claim 84 (Currently amended): The nucleic acid probe of claim [[82]] 75, wherein the oligonucleotide has at least 150 contiguous nucleotides having sequence identity to the nucleic acid target region.

Claim 85 (Currently amended): The nucleic acid probe of claim [[83]] 75, wherein the oligonucleotide has at least 200 contiguous nucleotides having sequence identity to the nucleic acid target region.

Claim 86 (Currently amended): The nucleic acid probe of claim [[84]] 75, wherein the oligonucleotide has a segment that is fully complementary to the nucleic acid target region.

Claim 87 (Canceled)

Claim 88 (Original): The nucleic acid probe of claim [[74]] 75, wherein the probe further comprises a detectable isotopic label.

Claim 89 (Original): The nucleic acid probe of claim [[74]] 75, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.

Claim 90 to 91 (Canceled)

sd-215892

Application No.: 10/081,872

13

Docket No.: 564462006100

Claim 92 (Currently amended): The nucleic acid probe of claim [[74]] 75, wherein the oligonucleotide hybridizes to the nucleic acid target region under stringent conditions to form a detectable target:probe duplex, wherein the stringent conditions comprise a wash step comprising 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution at Tm-10°C.

Claim 93 (Currently amended): A polynucleotide probe for isolation or identification of alpha amylase genes having a sequence which is the same as, or fully complementary to at least a [[35]] 50 nucleotide residue fragment of SEQ ID NO:125.

Claims 94 to 101 (Canceled)

Claim 102 (Currently amended): A cloning vector comprising a sequence that encodes a polypeptide having alpha amylase activity, said sequence comprising a sequence as set forth in claim 2 or claim 1, 10 or 12.

Claim 103 (Currently amended): A host cell comprising a nucleic acid having a sequence that encodes a polypeptide having alpha amylase activity, said sequence comprising a sequence as set forth in claim 2 or claim 1, 10 or 12.

Claim 104 (Currently amended): An expression vector capable of replicating in a host cell comprising a polynucleotide having a sequence as set forth in claim 2 or claim 1, 10 or 12.

Claim 105 (Currently amended): A vector as claimed in claim [[101]] 102, wherein the vector is selected from the group consisting of viral vectors, plasmid vectors, phage vectors, phagemid vectors, cosmids, fosmids, bacteriophages, artificial chromosomes, adenovirus vectors, retroviral vectors, and adeno-associated viral vectors.

sd-215892

Application No.: 10/081,872

14

Docket No.: 564462006100

Claim 106 (Currently amended): A host cell comprising an expression vector as claimed in claim [[102]] 104.

Claim 107 (Currently amended): A host cell as claimed in claim [[102]] 103, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, and plants.

Claim 108 (Currently amended): A method for liquifying a starch containing composition comprising contacting the starch with a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim ~~2-or-claim 1, 10 or 12~~.

Claims 109 to 111 (Canceled)

Claim 112 (Currently amended): A method for washing an object comprising contacting said object with a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim ~~2-or-claim 1, 10 or 12~~, under conditions sufficient for said washing.

Claim 113 (Currently amended): A method for textile desizing comprising contacting said textile with a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim ~~2-or-claim 1, 10 or 12~~, under conditions sufficient for said desizing.

Claim 114 (Currently amended): A method for the treatment of lignocellulosic fibers, wherein the fibers are treated with a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim ~~2-or-claim 1, 10 or 12~~, in an amount which is efficient for improving the fiber properties.

Claim 115 (Currently amended): A method according to claim 113 for enzymatic deinking of recycled paper pulp, wherein the polypeptide encoded by a nucleic acid comprising a

sd-215892

Application No.: 10/081,872

15

Docket No.: 564462006100

sequence as set forth in claim 2 or claim 1, 10 or 12 is applied in an amount which is efficient for effective deinking of the fiber surface.

Claim 116 (Currently amended): A method for starch liquefaction comprising contacting said starch with [[with]] a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim 2 or claim 1, 10 or 12 under conditions sufficient for said liquefaction.

Claim 117 (Canceled)

Claim 118 (Currently amended): A method for producing a high-maltose or a high-glucose syrup or a mixed syrup comprising:

liquefying starch using an effective amount of a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim 2 or claim 1, 10 or 12 to obtain a soluble starch hydrolysate; and

saccharifying the soluble starch hydrolysate, thereby resulting in a syrup.

Claim 119 (Currently amended): The method as in any of claims [[107]] 108, wherein the starch is from a material selected from rice, germinated rice, corn, barley, wheat, legumes and sweet potato.

Claim 120 (Currently amended): The method as in any of claims [[107]] 108, further comprising addition of a second alpha amylase or a beta amylase or a combination thereof.

Claim 121 (Currently amended): A method of increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging fluid formed during production operations and found within the subterranean formation which surrounds a completed well bore comprising:

allowing production fluids to flow from the well bore;

sd-215892

Application No.: 10/081,872

16

Docket No.: 564462006100

reducing the flow of production fluids from the formation below expected flow rates; formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide encoded by a nucleic acid comprising a sequence as set forth in claim 2 or ~~claim 1, 10 or 12;~~

pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, starch-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack the alpha glucosidic linkages in the starch-containing fluid.

Claim 122 (New): The method of claim 47, wherein the amino acid sequence has at least 97% sequence identity over a region of at least about 150 consecutive residues.

Claim 123 (New): The method of claim 47, wherein the amino acid sequence has at least 98% sequence identity over a region of at least about 100 or 150 consecutive residues.

Claim 124 (New): The method of claim 47, wherein the sequence identity is determined over the entire amino acid sequence.

sd-215892